

SCORE Search Results Details for Application 10552515 and Search Result 20080624_135830_us-10-552-515-1_copy_157_933.rup.

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This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_135830_us-10-552-515-1_copy_157_933.rup.

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GenCore version 6.2.1

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OM protein - protein search, using sw model

Run on: June 24, 2008, 15:17:39 ; Search time 529 Seconds
(without alignments)
2416.325 Million cell updates/sec

Title: US-10-552-515-1_COPY_157_933
Perfect score: 4123
Sequence: 1 QQDVQDGNTTVHYALLSASW.....SELSSHWTPFTVPKASQLQQ 777

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5032670 seqs, 1645091341 residues

Total number of hits satisfying chosen parameters: 5032670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_12.1:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4123	100.0	933	1 TM16G_HUMAN	Q6iwh7 homo sapien
2	3478.5	84.4	859	1 TM16G_MOUSE	Q14at5 mus musculus

3	3472	84.2	860	1	TM16G_RAT	Q6ift6	rattus norv
4	1505.5	36.5	920	2	A6QLE6_BOVIN	A6ql66	bos taurus
5	1498.5	36.3	955	1	TM16D_HUMAN	Q32m45	homo sapien
6	1476.5	35.8	903	2	Q1AP36_STRPU	Q1ap36	strongyloce
7	1475.5	35.8	921	2	Q1AP35_STRPU	Q1ap35	strongyloce
8	1472	35.7	981	2	A2AHE5_MOUSE	A2ahe5	mus musculu
9	1467.5	35.6	981	1	TM16C_HUMAN	Q9byt9	homo sapien
10	1463	35.5	900	2	A1A5Z4_DANRE	A1a5z4	danio rerio
11	1460.5	35.4	921	2	Q1AP37_STRPU	Q1ap37	strongyloce
12	1452.5	35.2	960	1	TM16A_MOUSE	Q8bhy3	mus musculu
13	1450.5	35.2	986	1	TM16A_HUMAN	Q5xxa6	homo sapien
14	1437	34.9	999	1	TM16B_HUMAN	Q29nq9	homo sapien
15	1434.5	34.8	913	2	Q8CFW1_MOUSE	Q8cfw1	mus musculu
16	1419	34.4	896	2	Q6DDQ3_XENLA	Q6ddq3	xenopus lae
17	1413.5	34.3	1014	2	Q175J3_AEDAE	Q175j3	aedes aegyp
18	1413.5	34.3	1117	2	Q0IEX5_AEDAE	Q0iex5	aedes aegyp
19	1412.5	34.3	913	1	TM16E_HUMAN	Q75v66	homo sapien
20	1402.5	34.0	906	2	Q7QDY0_ANOGA	Q7qdy0	anopheles g
21	1382.5	33.5	412	2	Q4SC97_TETNG	Q4sc97	tetraodon n
22	1382.5	33.5	1235	2	Q2M0Y5_DROPS	Q2m0y5	drosophila
23	1378.5	33.4	1219	2	Q9VTS0_DROME	Q9vts0	drosophila
24	1369	33.2	910	1	TM16F_HUMAN	Q4kmq2	homo sapien
25	1367.5	33.2	712	2	Q8NCT7_HUMAN	Q8nct7	homo sapien
26	1366.5	33.1	1613	2	Q4S1F6_TETNG	Q4s1f6	tetraodon n
27	1355.5	32.9	909	2	A6NNM6_HUMAN	A6nnm6	homo sapien
28	1351	32.8	904	1	TM16E_MOUSE	Q75ur0	mus musculu
29	1351	32.8	904	2	Q3V657_MOUSE	Q3v657	mus musculu
30	1346	32.6	871	2	Q8JFT1_DANRE	Q8jft1	danio rerio
31	1344	32.6	926	2	Q8IN71_DROME	Q8in71	drosophila
32	1344	32.6	1075	2	Q9VDV4_DROME	Q9vdrv4	drosophila
33	1343	32.6	972	2	Q86P24_DROME	Q86p24	drosophila
34	1336.5	32.4	911	1	TM16F_MOUSE	Q6p9j9	mus musculu
35	1329	32.2	1062	2	Q293M2_DROPS	Q293m2	drosophila
36	1291	31.3	895	2	Q16L02_AEDAE	Q16l02	aedes aegyp
37	1290	31.3	1035	2	Q4SSV5_TETNG	Q4ssv5	tetraodon n
38	1281	31.1	863	2	Q16MH2_AEDAE	Q16mh2	aedes aegyp
39	1251.5	30.4	823	2	Q7QEP9_ANOGA	Q7qep9	anopheles g
40	1227.5	29.8	971	2	Q4REV7_TETNG	Q4rev7	tetraodon n
41	1221	29.6	1017	2	Q29H97_DROPS	Q29h97	drosophila
42	1207	29.3	984	2	Q8MT62_DROME	Q8mt62	drosophila
43	1205	29.2	854	2	Q2VPA8_MOUSE	Q2vpa8	mus musculu
44	1159.5	28.1	1043	2	Q9VYS8_DROME	Q9vys8	drosophila
45	1159.5	28.1	1059	2	Q76NS2_DROME	Q76ns2	drosophila

ALIGNMENTS

RESULT 1

TM16G_HUMAN

ID TM16G_HUMAN Reviewed; 933 AA.

AC Q6IWH7; Q6IWH6;

DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.

DT 05-JUL-2004, sequence version 1.

DT 24-JUL-2007, entry version 21.

DE Transmembrane protein 16G (New gene expressed in prostate) (Prostate

DE cancer-associated protein 5) (IPCA-5) (Dresden-transmembrane protein
DE of the prostate) (D-TMPP).

GN Name=TMEM16G; Synonyms=NGEP, PCANAP5;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), TISSUE SPECIFICITY,
RP SUBCELLULAR LOCATION, AND TOPOLOGY.
RX PubMed=14981236; DOI=10.1073/pnas.0308746101;
RA Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,
RA Hahn Y., Lee B., Pastan I.;
RT "NGEP, a gene encoding a membrane protein detected only in prostate
RT cancer and normal prostate.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:3059-3064(2004).
RN [2]
RP IDENTIFICATION.
RX PubMed=10613842; DOI=10.1101/gr.9.12.1198;
RA Walker M.G., Volkmuth W., Sprinzak E., Hodgson D., Klingler T.;
RT "Prediction of gene function by genome-scale expression analysis:
RT prostate cancer-associated genes.";
RL Genome Res. 9:1198-1203(1999).
RN [3]
RP IDENTIFICATION.
RX PubMed=15375614;
RA Katoh M., Katoh M.;
RT "Characterization of human TMEM16G gene in silico.";
RL Int. J. Mol. Med. 14:759-764(2004).
RN [4]
RP ALTERNATIVE SPLICING (ISOFORM 3), TISSUE SPECIFICITY, AND INDUCTION BY
RP ANDROGEN.
RX PubMed=15761874; DOI=10.1002/pros.20250;
RA Kiessling A., Weigle B., Fuessel S., Ebner R., Meye A., Rieger M.A.,
RA Schmitz M., Temme A., Bachmann M., Wirth M.P., Rieber E.P.;
RT "D-TMPP: a novel androgen-regulated gene preferentially expressed in
RT prostate and prostate cancer that is the first characterized member of
RT an eukaryotic gene family.";
RL Prostate 64:387-400(2005).
RN [5]
RP FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX PubMed=17308099; DOI=10.1158/0008-5472.CAN-06-2673;
RA Das S., Hahn Y., Nagata S., Willingham M.C., Bera T.K., Lee B.,
RA Pastan I.;
RT "NGEP, a prostate-specific plasma membrane protein that promotes the
RT association of LNCaP cells.";
RL Cancer Res. 67:1594-1601(2007).
CC -!- FUNCTION: May play a role in cell-cell interactions.
CC -!- SUBCELLULAR LOCATION: Isoform 1: Cell membrane; Multi-pass
CC membrane protein. Isoform 2: Cytoplasm, cytosol. Note=Isoform 1
CC concentrates at sites of cell-cell contact.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=NGEP-L;

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CC      IsoId=Q6IWH7-1; Sequence=Displayed;
CC      Name=2; Synonyms=NGEP-S;
CC      IsoId=Q6IWH7-2; Sequence=VSP_026004, VSP_026005, VSP_026006;
CC      Name=3; Synonyms=D-TMPP;
CC      IsoId=Q6IWH7-3; Sequence=VSP_026004, VSP_026007, VSP_026008;
CC      -!- TISSUE SPECIFICITY: Specifically expressed in epithelial cells of
CC      the prostate (at protein level).
CC      -!- INDUCTION: Up-regulated by androgen.
CC      -!- SIMILARITY: Belongs to the TMEM16 family.
CC      -!- CAUTION: It is uncertain whether Met-1 or Met-55 is the initiator.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AY617079; AAT40139.1; -; mRNA.
DR      EMBL; AY617080; AAT40140.1; -; mRNA.
DR      UniGene; Hs.163909; -.
DR      Ensembl; ENSG00000146205; Homo sapiens.
DR      HGNC; HGNC:31677; TMEM16G.
DR      MIM; 605096; gene.
DR      PharmGKB; PA32980; -.
DR      ArrayExpress; Q6IWH7; -.
DR      GO; GO:0005886; C:plasma membrane; IDA:MGI.
DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      1: Evidence at protein level;
KW      Alternative splicing; Cytoplasm; Membrane; Polymorphism;
KW      Transmembrane.
FT      CHAIN          1           933           Transmembrane protein 16G.
FT                                     /FTId=PRO_0000289326.
FT      TOPO_DOM        1           355           Extracellular (Potential).
FT      TRANSMEM        356         376           Potential.
FT      TOPO_DOM        377         420           Cytoplasmic (Potential).
FT      TRANSMEM        421         441           Potential.
FT      TOPO_DOM        442         499           Extracellular (Potential).
FT      TRANSMEM        500         520           Potential.
FT      TOPO_DOM        521         550           Cytoplasmic (Potential).
FT      TRANSMEM        551         571           Potential.
FT      TOPO_DOM        572         588           Extracellular (Potential).
FT      TRANSMEM        589         609           Potential.
FT      TOPO_DOM        610         714           Cytoplasmic (Potential).
FT      TRANSMEM        715         735           Potential.
FT      TOPO_DOM        736         763           Extracellular (Potential).
FT      TRANSMEM        764         784           Potential.
FT      TOPO_DOM        785         843           Cytoplasmic (Potential).
FT      TRANSMEM        844         864           Potential.
FT      TOPO_DOM        865         933           Extracellular (Potential).
FT      VAR_SEQ         110         110           Missing (in isoform 2 and isoform 3).
FT                                     /FTId=VSP_026004.
FT      VAR_SEQ         158         180           QDVQDGNITTVHYALLSASWAVLC -> VRGGCHGQGPRPCI
FT      HSVTHDLAA (in isoform 2).
FT                                     /FTId=VSP_026005.
FT      VAR_SEQ         181         933           Missing (in isoform 2).
FT      HSVTHDLAA (in isoform 2).
FT                                     /FTId=VSP_026006.
FT      VAR_SEQ         859         859           H -> VAEAPAGSPIHGMRPRPCALPNSSTW (in

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FT isoform 3).

FT /FTId=VSP_026007.

FT VAR_SEQ 860 933 Missing (in isoform 3).

FT /FTId=VSP_026008.

FT VARIANT 67 67 V -> I (in dbSNP:rs2302054).

FT /FTId=VAR_032616.

SQ SEQUENCE 933 AA; 105531 MW; D6FD42578A41D7D3 CRC64;

Query Match 100.0%; Score 4123; DB 1; Length 933;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQDVQDGNITTVHYALLSASWAVLCYYAEDLRLKLPQLQELPNQASNWSAGLLAWLGIPNVL 60
 |||

Db 157 QQDVQDGNITTVHYALLSASWAVLCYYAEDLRLKLPQLQELPNQASNWSAGLLAWLGIPNVL 216

Qy 61 LEVVPDVPPEYYSCRFRVKNLPRFLGSDNQDTFTTSTKRHQILFEILAKTPYGHEKKNL 120
 |||

Db 217 LEVVPDVPPEYYSCRFRVKNLPRFLGSDNQDTFTTSTKRHQILFEILAKTPYGHEKKNL 276

Qy 121 GIHQLLAEGVLSAAFLPHDGPFTKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
 |||

Db 277 GIHQLLAEGVLSAAFLPHDGPFTKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 336

Qy 181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 240
 |||

Db 337 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL 396

Qy 241 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 300
 |||

Db 397 CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSD 456

Qy 301 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVMCLV 360
 |||

Db 457 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVMCLV 516

Qy 361 SIILYRAIMAVVSRSGNTLLAAWASRIASLTGSSVNLVLFILILSKIYVSLAHVLTREW 420
 |||

Db 517 SIILYRAIMAVVSRSGNTLLAAWASRIASLTGSSVNLVLFILILSKIYVSLAHVLTREW 576

Qy 421 HRTQTKFEDAFLKVFIFQFVN FYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 480
 |||

Db 577 HRTQTKFEDAFLKVFIFQFVN FYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC 636

Qy 481 LIELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFLRSKKRKAGASAGASQGPWEDDY 540
 |||

Db 637 LIELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFLRSKKRKAGASAGASQGPWEDDY 696

Qy 541 ELVPC EGLFDEYLEMVLQFGVTFIFVAACPLAPL FALLNNWVEIRLDARKFVCEYRPPVA 600
 |||

Db 697 ELVPC EGLFDEYLEMVLQFGVTFIFVAACPLAPL FALLNNWVEIRLDARKFVCEYRPPVA 756

Qy 601 ERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYYRWTRAHDLRGLFNFTLARAP 660
 |||

Db 757 ERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYYRWTRAHDLRGLFNFTLARAP 816

```

Qy      661 SSFAAAHNRTCryAFRDDDDGHYSQTYWNLALAIRLAFVIVFEHVVSFVGRLLDLLVPDIP 720
      |||
Db      817 SSFAAAHNRTCryAFRDDDDGHYSQTYWNLALAIRLAFVIVFEHVVSFVGRLLDLLVPDIP 876

Qy      721 ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ 777
      |||
Db      877 ESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ 933

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RESULT 2

TM16G_MOUSE

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ID      TM16G_MOUSE      Reviewed;      859 AA.
AC      Q14AT5; Q6IFT5;
DT      29-MAY-2007, integrated into UniProtKB/Swiss-Prot.
DT      29-MAY-2007, sequence version 2.
DT      24-JUL-2007, entry version 9.
DE      Transmembrane protein 16G (New gene expressed in prostate homolog).
GN      Name=Tmem16g; Synonyms=Ngep;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muroidea; Muridae; Murinae; Mus.
OX      NCBITaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=C57BL/6J;
RG      The mouse genome sequencing consortium;
RL      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RX      PubMed=15489334; DOI=10.1101/gr.2596504;
RG      The MGC Project Team;
RT      "The status, quality, and expansion of the NIH full-length cDNA
RT      project: the Mammalian Gene Collection (MGC).";
RL      Genome Res. 14:2121-2127(2004).
RN      [3]
RP      IDENTIFICATION.
RX      PubMed=14981236; DOI=10.1073/pnas.0308746101;
RA      Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,
RA      Hahn Y., Lee B., Pastan I.;
RT      "NGEP, a gene encoding a membrane protein detected only in prostate
RT      cancer and normal prostate.";
RL      Proc. Natl. Acad. Sci. U.S.A. 101:3059-3064(2004).
CC      -!- FUNCTION: May play a role in cell-cell interactions (By
CC      similarity).
CC      -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein
CC      (By similarity). Note=Concentrates at sites of cell-cell contact
CC      (By similarity).
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=Q14AT5-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q14AT5-2; Sequence=VSP_026009, VSP_026010;
CC      -!- SIMILARITY: Belongs to the TMEM16 family.

```


Db	219	GIDQLLAEGVFSAAFPLHDGPFSAVDESSQVLGLIQRQVLFQHWARWGKNKYQPLDHVR	278
Qy	181	RYFG EKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL	240
Db	279	RYFG EKVALYFAWLGFYTGWLLPAAVVGTVVFLVGCFLVFSDIPTQELCHSSDSFDMCPL	338
Qy	241	CLDCPFWLLSSACALAQAGRLFDHG GTVFFSLFMALWAVL LLEYWKRKSATLAYRWDCSD	300
Db	339	CSDCSFWLLSSACTLAQAGRLFDHG GTVFFSLFMALWAVL LLEYWKRKNATLAYRWDCSD	398
Qy	301	YEDTEERPRPQFAASAPMTAPNPTIGDEDEPYFPERSRARRMLAGSVVIVVMVAVVMCLV	360
Db	399	YEDIEERPRPQFAATAPMTALNPITIGDEDEPYFPEKNRVRRLAGSVVLLMMVAVVMCLV	458
Qy	361	SIILYRAIMAVVSRSGNTLLAAWASRIASLTGSSVVNVLVFLILSKYIVSLAHVLTWRWEM	420
Db	459	SVILYRAVMIIIVSRSDNAFLSAWASRIASLTGSSVVNVLVFLILSKVYVLLAQVLTWRWEM	518
Qy	421	HRTQTKEFDAFTLKFVIFQFVN FYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC	480
Db	519	HRTQTEFDAFTLKFVIFQFVN FYASPVYIAFFKGRFVGYPGNYHTLFGIRNEEC PAGGC	578
Qy	481	LIELAQELLVIMVGKQVINNMQEVLPKLGKWWQKFLRSKKRKAGASAGASQGPWEDDY	540
Db	579	LSLAEQELLVIMVGKQIINN VQEVLPVKLGKCWQKF---SRGKKAG--TGTHPAPWEADY	633
Qy	541	ELVPCEGLFDEYLEMVLQFGVTFIVFAACPLAPL FALLNNWVEIRLDARKFVCEYRRPVA	600
Db	634	ELLPCEGLFHEYLEMVLQFGVTFIVFAACPLAPL FALLNNWVEIRLDARKFVCEYRRPVA	693
Qy	601	ERAQDIGIWFHILAGLTHLAVISNAFL LAFSSDFLPRAYYRWTRAHDLRGLNFTLARAP	660
Db	694	ERAQDIGIWFHILTLGLTHLAVISNAFL LAFSSDFLPRVYYSWTHAPDLHGLNFTLARAP	753
Qy	661	SSFAAAHNRTCRYRAFRDDDGHSYQTYWNLLAIRLAFVIVFEHV VFSVGRLLDLLVPDIP	720
Db	754	PTFTSAHNRTCRYRAFRDDDGHSPTYTWLLAIRLAFVIVFEHV VFSIGRVLLDLLVPDIP	813
Qy	721	ESVEIKVKREYYLAKQALAE NEVLFGTNGTKDEQPKGSELS	761
Db	814	ESVEIKVKREYYLAKOALAE NEALLGATGVKDDOPPSSSEPS	854

RESULT 3

TM16G RAT

```
ID      TM16G_RAT                      Reviewed;          860 AA.
AC      Q6IFT6;
DT      29-MAY-2007, integrated into UniProtKB/Swiss-Prot.
DT      05-JUL-2004, sequence version 1.
DT      24-JUL-2007, entry version 22.
DE      Transmembrane protein 16G (New gene expressed in prostate homolog).
GN      Name=Imem16g; Synonyms=Ngep;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muroidea; Muridae; Murinae; Rattus.
```


OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Brown Norway;
 RX PubMed=15057822; DOI=10.1038/nature02426;
 RA Gibbs R.A., Weinstock G.M., Metzker M.L., Muzny D.M., Sodergren E.J.,
 RA Scherer S., Scott G., Steffen D., Worley K.C., Burch P.E., Okwuonu G.,
 RA Hines S., Lewis L., Deramo C., Delgado O., Dugan-Rocha S., Miner G.,
 RA Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,
 RA Baden-Tillson H., Barnstead M., Chin S., Evans C.A., Ferriera S.,
 RA Fosler C., Glodek A., Gu Z., Jennings D., Kraft C.L., Nguyen T.,
 RA Pfannkoch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T.,
 RA Smith D., Lee H.-M., Gustafson E., Cahill P., Kana A.,
 RA Doucette-Stamm L., Weinstock K., Fechtel K., Weiss R.B., Dunn D.M.,
 RA Green E.D., Blakesley R.W., Bouffard G.G., De Jong P.J., Osoegawa K.,
 RA Zhu B., Marra M., Schein J., Bosdet I., Fjell C., Jones S.,
 RA Krzywinski M., Mathewson C., Siddiqui A., Wye N., McPherson J.,
 RA Zhao S., Fraser C.M., Shetty J., Shatsman S., Geer K., Chen Y.,
 RA Abramson S., Nierman W.C., Havlak P.H., Chen R., Durbin K.J., Egan A.,
 RA Ren Y., Song X.-Z., Li B., Liu Y., Qin X., Cawley S., Cooney A.J.,
 RA D'Souza L.M., Martin K., Wu J.Q., Gonzalez-Garay M.L., Jackson A.R.,
 RA Kalafus K.J., McLeod M.P., Milosavljevic A., Vink D., Volkov A.,
 RA Wheeler D.A., Zhang Z., Bailey J.A., Eichler E.E., Tuzun E.,
 RA Birney E., Mongin E., Ureta-Vidal A., Woodwark C., Zdobnov E.,
 RA Bork P., Suyama M., Torrents D., Alexandersson M., Trask B.J.,
 RA Young J.M., Huang H., Wang H., Xing H., Daniels S., Gietzen D.,
 RA Schmidt J., Stevens K., Vitt U., Wingrove J., Camara F., Mar Alba M.,
 RA Abril J.F., Guigo R., Smit A., Dubchak I., Rubin E.M., Couronne O.,
 RA Poliakov A., Huebner N., Ganten D., Goesele C., Hummel O.,
 RA Kreitler T., Lee Y.-A., Monti J., Schulz H., Zimdahl H.,
 RA Himmelbauer H., Lehrach H., Jacob H.J., Bromberg S.,
 RA Gullings-Handley J., Jensen-Seaman M.I., Kwitek A.E., Lazar J.,
 RA Pasko D., Tonellato P.J., Twigger S., Ponting C.P., Duarte J.M.,
 RA Rice S., Goodstadt L., Beaton S.A., Emes R.D., Winter E.E.,
 RA Webber C., Brandt P., Nyakatura G., Adetobi M., Chiaromonte F.,
 RA Elnitski L., Eswara P., Hardison R.C., Hou M., Kolbe D., Makova K.,
 RA Miller W., Nekrutenko A., Riemer C., Schwartz S., Taylor J., Yang S.,
 RA Zhang Y., Lindpaintner K., Andrews T.D., Caccamo M., Clamp M.,
 RA Clarke L., Curwen V., Durbin R.M., Eyas E., Searle S.M., Cooper G.M.,
 RA Batzoglou S., Brudno M., Sidow A., Stone E.A., Payseur B.A.,
 RA Bourque G., Lopez-Otin C., Puente X.S., Chakrabarti K., Chatterji S.,
 RA Dewey C., Pachter L., Bray N., Yap V.B., Caspi A., Tesler G.,
 RA Pevzner P.A., Haussler D., Roskin K.M., Baertsch R., Clawson H.,
 RA Furey T.S., Hinrichs A.S., Karolchik D., Kent W.J., Rosenbloom K.R.,
 RA Trumbower H., Weirauch M., Cooper D.N., Stenson P.D., Ma B., Brent M.,
 RA Arumugam M., Shteynberg D., Copley R.R., Taylor M.S., Rietman H.,
 RA Mudunuri U., Peterson J., Guyer M., Felsenfeld A., Old S., Mockrin S.,
 RA Collins F.S.;
 RT "Genome sequence of the Brown Norway rat yields insights into
 RT mammalian evolution."
 RL Nature 428:493-521(2004).
 RN [2]
 RP IDENTIFICATION.
 RX PubMed=14981236; DOI=10.1073/pnas.0308746101;
 RA Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,


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Db      159  LENVPDTPPEYYSCQFKASKLQWFLGSDNQDTFTTSTKRHQILFEILAKTPYGHQKGLF  218
Qy      121  GIHQLLAEGVLSAAAPFLHDGPFKTPPEGPAAPRLNQRQVLFQHWARWGKWNKYQPLDHR  180
Db      219  GIDQLLAEGVLSAAAPFLHDGPFVVPPESSQVLGLTQRQVLFKHWARWGKWRKYQPLDHR  278
Qy      181  RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPL  240
Db      279  RYFGEKVALYFAWLGFYTGWLLPAAVVGTVVFLAGCFLVFSDVPTQELCHSSDTFDMCPL  338
Qy      241  CLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLELYWKRKSATLAYRWD CSD  300
Db      339  CSDCSFWLLSSACTLAQAGRLFDHGGTVFFSLFMALWAVLLELYWKRKNATLAYRWD CSD  398
Qy      301  YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPPERSARRMLAGSVVIVMVAVVMCLV  360
Db      399  YEDIEERPRPQFAATAPMTALNPITGEDEPYFPEKNRVRRLAGSVVLLMMVAVVMCLV  458
Qy      361  SIILYRAIMAIIVSRSGNTLLAAWASRIASLTGSVVNLVLFILILSKIYVSLAHVLRWEM  420
Db      459  SIILYRAVMAIIVSKSNNAFSLAWASRIASLTGSVVNLVLFILILSKVYVILAQVLRWEM  518
Qy      421  HRTQTKFEDAFTLKVIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGC  480
Db      519  HRTQTAFEDAFTLKVIFQFVNIFYASPVYIAFFKGRFVGYPGNYHTLFGVRNEECAGGC  578
Qy      481  LIELAQELLVIMVGKQVINNMQEVLIPLKLGWQKFLRLSKRRKAGASAGASQGPWEDDY  540
Db      579  LSELAQELLVIMVGKQIINNVEVLVPLKKGWQK--LCSRRKAG--MGANPAPWEADY  634
Qy      541  ELVPCGFLFDEYLEMVLQFGVTFIFVAACPLAPLALLNNWVEIRLDARFVCEYRRPVA  600
Db      635  ELLPCGFLFHEYLEMVLQFGVTFIFVAACPLAPLALLNNWVEIRLDARFVCEYRRPVA  694
Qy      601  ERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYYRWTRAHDLRGLNFTLARAP  660
Db      695  ERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRVYYSWTRAPDLRGLNFTLARAP  754
Qy      661  SSFAAAHNRTCryRAFRDDDGHSYQTYWNLALAIRLAFVIVFEHVVFVSGRLLDLLVPDIP  720
Db      755  PTFTSAHNRTCryRAFRDDDGHSYPTYWTLALAIRLAFVIVFEHVVFSTGRFLDLLVPDIP  814
Qy      721  ESVEIKVKREYLLAKQALANEVLFGTNGTKDEQPKGSLS  761
Db      815  ESVEIKVKREYLLAKQALADNEALGATGVKGEQPPSSEPS  855

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RESULT 4

A6QLE6_BOVIN

ID A6QLE6_BOVIN

Unreviewed;

920 AA.

AC A6QLE6;

DT 21-AUG-2007, integrated into UniProtKB/TrEMBL.

DT 21-AUG-2007, sequence version 1.

DT 21-AUG-2007, entry version 1.

DE Putative uncharacterized protein.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=L1 Hereford; TISSUE=Basal ganglia;
 RA Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
 RA Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
 RA Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
 RA Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
 RA Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
 RA Siddiqui A., Holt R., Jones S.J., Marra M.A.;
 RL Submitted (JUN-2007) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; BC147937; AAI47938.1; -; mRNA.
 PE 2: Evidence at transcript level;
 SQ SEQUENCE 920 AA; 107708 MW; 3AFFC6310F1862CD CRC64;

Query Match 36.5%; Score 1505.5; DB 2; Length 920;
 Best Local Similarity 40.4%; Pred. No. 1.6e-116;
 Matches 328; Conservative 145; Mismatches 270; Indels 69; Gaps 20;

Qy 8 NTTVHYALLSASWAVLCYYAEDLRLKLPQE----LPNQASNWS-----AGLLAWLGIP 57
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 Db 122 NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRKRIYYLPRRYKFSRIDKQISRFRRLWPKK 181
 Qy 58 NVLL--EVPVDVPP-EYYSRFRVKNLPRFLGSDNQDITFTSTKRHQILFEILAKTPYGH 114
 : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
 Db 182 PMRLDKETLPDLEENDCYTAPFSQQRHFFI- IHNKDTFFNNATRSRIVHHILQRIKY-E 239
 Qy 115 EKKNLLGIHQLLAEGVLSAFAFLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWKYQ 174
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 Db 240 EGKNKIGLNRLLTNGSYEAFAFLHEGSYRSKNSIRTHGAVNHRHLLYECWASWGVVWKYQ 299
 Qy 175 PLDHVRRYFGEKVALYFAWLGFTYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDS 234
 | | | | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 300 PLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLFVFLYGVITLDHCQVSKEVCQATDI 359
 Qy 235 FEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMLAWALLLEYWKRKSATLA 293
 | | : | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 360 I-MCPVCDKYCPFMRSLSDSCVYAKVTHLFDNGATVFFAVFMAVWATVFLFVWKRRAVIA 418
 Qy 294 YRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLGASVVIVVMV 352
 : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
 Db 419 YDWDLIDWEEEEERIPQFEAKYSKKERMNPISGKPEPYQAFADKCSRLIVSASGIFFMI 478
 Qy 353 AVVVMCLVSIILYRAIMAVVSRSGNTLLA-AWA-----SRIASLTGSVV--NLVFILIL 404
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 Db 479 CVVIAAVFGVIYIRVVTV-----STFAAFKQWALIRNNSQVAT-TGTAVCINFCIIMLL 530

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RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigetani K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA
RT project: the Mammalian Gene Collection (MGC).";
RL Genome Res. 14:2121-2127(2004).
RN [3]
RP IDENTIFICATION.
RX PubMed=12739008;
RA Katoh M., Katoh M.;
RT "FLJ10261 gene, located within the CCND1-EMS1 locus on human
RT chromosome 11q13, encodes the eight-transmembrane protein homologous
RT to C12orf3, C11orf25 and FLJ34272 gene products.";
RL Int. J. Oncol. 22:1375-1381(2003).
CC -!- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein
CC (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q32M45-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q32M45-2; Sequence=VSP_025742;
CC Name=3;
CC IsoId=Q32M45-3; Sequence=VSP_025741, VSP_025743;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the TMEM16 family.

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CC -----
DR EMBL; AK091540; BAC03688.1; ALT_INIT; mRNA.
DR EMBL; AK091591; BAC03704.1; -; mRNA.

DR EMBL; AK092596; BAC03924.1; -; mRNA.
 DR EMBL; BC109308; AA109309.1; -; mRNA.
 DR UniGene; Hs.58785; -.
 DR Ensembl; ENSG00000151572; Homo sapiens.
 DR HGNC; HGNC:23837; TMEM16D.
 DR MIM; 610111; gene.
 DR PharmGKB; PA134975112; -.
 DR ArrayExpress; Q32M45; -.
 DR InterPro; IPR007632; DUF590.
 DR PANTHER; PTHR12308; DUF590; 1.
 DR Pfam; PF04547; DUF590; 1.
 PE 2: Evidence at transcript level;
 KW Alternative splicing; Coiled coil; Glycoprotein; Membrane;
 KW Polymorphism; Transmembrane.

FT	CHAIN	1	955	Transmembrane protein 16D. /FTId=PRO_0000288650.
FT	TRANSMEM	353	373	Potential.
FT	TRANSMEM	425	445	Potential.
FT	TRANSMEM	506	526	Potential.
FT	TRANSMEM	548	568	Potential.
FT	TRANSMEM	596	616	Potential.
FT	TRANSMEM	716	736	Potential.
FT	TRANSMEM	769	789	Potential.
FT	TRANSMEM	886	906	Potential.
FT	COILED	918	953	Potential.
FT	CARBOHYD	824	824	N-linked (GlcNAc. . .) (Potential).
FT	VAR_SEQ	1	433	Missing (in isoform 3). /FTId=VSP_025741.
FT	VAR_SEQ	19	54	EGGVDLQGYQLDMQILPDGPKSDVDFSEILNAIQEM -> V (in isoform 2). /FTId=VSP_025742.
FT	VAR_SEQ	466	512	Missing (in isoform 3). /FTId=VSP_025743.
FT	VARIANT	115	115	G -> A (in dbSNP:rs34162417). /FTId=VAR_032453.
FT	CONFLICT	209	209	F -> L (in Ref. 1; BAC03704).
SQ	SEQUENCE	955 AA;	111462 MW;	9A9348C61A4F20AF CRC64;

Query Match 36.3%; Score 1498.5; DB 1; Length 955;
 Best Local Similarity 40.3%; Pred. No. 6.4e-116;
 Matches 327; Conservative 145; Mismatches 271; Indels 69; Gaps 20;

Qy	8	NTTVHYALLSASWAVLCYYAEDLRKLPLQE----	LPNQASNWS-----	AGLLAWLGIP	57
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Db	157	NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRKRIYYLPRRYKFMRSIDKQISRFRRLPKK	216		
Qy	58	NVLL--EVVPDPPP--EYYSRCFRVKNLPRFLGSDNQDTFTSTKRHQILFEILAKTPYGH	114		
		: : : : : : : : : : :			
Db	217	PMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNATRSRIVHHILQRIKY-E	274		
Qy	115	EKKNLLGIHQLLAEGVLSAAFLHDGPFKTPPEGPQAPRLNQRQVLQFQHWARWGKWKYQ	174		
		: : : : : : : :			
Db	275	EGKNKIGLNRLLTNGSYEAAFLPEGYSYRSKNSIRTHGAENHRHLLYECWASGWVWYKYQ	334		
Qy	175	PLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDS	234		

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Db      335  ||| |||||:|: |||||:| | || |: | ||| | : :||:| : |
Qy      235  PLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLGFVFLYGVTTLDHSQVSKEVCQATDI 394
Db      395  |||:| ||| || |: | |||:| |||:| |||:| |: |||:| |:|
Qy      294  I-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFAVFMAVWATVFLEFWKRRRAVIA 453
Db      454  YDWDLIDWEEEEIEIRPQFEAKYSKKERMNPISGKPEPYQAFDTKCSRLIVSASGIFFMI 513
Qy      353  AVVVMCLVSIILYRAIMAIVVSRSGNTLLA-AWA-----SRIASLTGSSV--NLVFILIL 404
Db      514  ||: : ||:| | ||| | : |||:| ||| : ||: : | |:|
Qy      405  CVVIAAVFGIVIRVVTV-----STFAAFKWLIRNNSQVAT-TGTAVCINFCIIMLL 565
Db      566  SKIYVSLAHVLRWEMHRTQTKFEDAFTLKVFIQFVNIFYSSPVYIAFFKGRFVGYPGNY 625
Qy      465  NVLYEKVALLLTNLQPRTESEWENSFTLKMFLQFVNLNSSTFYIAFFLGRFTGHPGAY 625
Db      626  HTLFG--VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFLRLSKKR 523
Qy      524  | | ||| ||||:| :::| || | | |: | :::| | ::
Db      683  LRLINRWRLEECHPSGCLIDLQMGIIMVLKQTWNFMELGYPLIQNWVTR---RKVRQ 682
Qy      582  KAGASAGASQGPWEDDYELVPC--GLFDEYLEMVLQFGFVTIFVAAACPLAPLALLNNW 811
Db      683  | : | | | | |||||:| ||| | ||||| | ||||| | |||||
Qy      582  EHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGTTTFVAAFFLAPLALLNNI 742
Db      743  VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYR 841
Qy      642  : ||||| || : |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db      803  IEIRLDAYKFVTQWRRLASRAKDIGIWIYGILEGIGILSVITNAFVIAITSDFIPRLVYA 802
Qy      642  W-----TRAHDLRGFLNFTLA-----RAPSSFAAAHNRTCRYRAFR 677
Db      803  : : ||:| |:| : |||:| | |: : |||:| |
Qy      678  YKYGPCAGQGEAGQKCMGVYNASLSVFRISDFENRSEPSDGESEFSGTPLYCRYRDYR 862
Db      863  DDDGH-----YSQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYY 732
Qy      733  | |: : ||| | |||:| |||:| |||:| |||:| |||:| |||:|
Db      923  DPPHSLVPYGYTLQFVHVLAARLAFIIVFEHLVFCIKHLISYLIPDLPKLDRDRMRREKY 922
Qy      733  LAKQALANEVLFGTNGTKDEQPKGSELSSHW 764
Db      923  | :: : | |: | : | : |
Qy      923  LIQEMMYEAELERLQKERKKNKKAHHNEW 954

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RESULT 6

Q1AP36_STRPU

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ID      Q1AP36_STRPU      Unreviewed;      903 AA.
AC      Q1AP36;
DT      11-JUL-2006, integrated into UniProtKB/TrEMBL.
DT      11-JUL-2006, sequence version 1.
DT      24-JUL-2007, entry version 6.
DE      122 kDa protein TMEM16 (Fragment).
OS      Strongylocentrotus purpuratus (Purple sea urchin).
OC      Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC      Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC      Strongylocentrotus.

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Db      526 NLELHRTETEDYSFTFKMYLFAFVNYSTSFYIAFFKGRPLPGTPADYGRVFGIWRQEEC 585
Qy      476 AAGGCLIELAQELLVIMVGQKVINNMQEVLPKLGWQKFRRLSKRRKAGASAGASQGP 535
      ||: || : : ||| || |: :| | |: | |: ||
Db      586 DPAGCMQELFINIAITMCGKQFFNNFMELAMPVLMNFWRS-RTGRKEEKESGK---GRYEQ 641
Qy      536 WEDDYELVPC---EGLFDEYLEMVLQFGFVTIFVAACPLAPLALLNNWVEIRLDARKFVC 593
      || | :| ||| |||||:|||| ||||| ||||| |||:|||| ||:
Db      642 WEQDADLADLGPRLGFKEYLEMVVQFGFSTIFVAAFPLAPLALLNNLVEVRLDAYKFIS 701
Qy      594 EYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPR---AYYRWTRAHDLRG 650
      : |||||:||||| |: || : :|:|:| :||:|:|:| || | |
Db      702 QLRRPVAKRAQDIGAWYAILVTVGNLVLTNALVIAFTSEFIPQVQFKYYYGGPEATLNG 761
Qy      651 FLNFTLA-----RAPSSFAAAHNRT-----CRYRAFRDDDDGHYSQT 686
      : ||:|: || | ||| |: ||: |
Db      762 YTNWSLSYFNTVDMQNDKSKPTDPSYPRVGDEDTTDPNYGLNVSVCRYRGNYDE---HYNVT 819
Qy      687 --YWNLLAIRLAFVIVFEHVSVGRLLDLLVPDIPESVEIKVKREYYLAKQAL 738
      || :||:|:|:|:|:| | : :||:| | : :||| || :|||
Db      820 LDYWLVIKIAKLAIFILLYEHFVLFKFFVAYIIPDMPEFVNQIKRETYLGQQAL 873

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RESULT 7

Q1AP35_STRPU

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ID      Q1AP35_STRPU              Unreviewed;          921 AA.
AC      Q1AP35;
DT      11-JUL-2006, integrated into UniProtKB/TrEMBL.
DT      11-JUL-2006, sequence version 1.
DT      24-JUL-2007, entry version 6.
DE      122 kDa protein TMEM16.
OS      Strongylocentrotus purpuratus (Purple sea urchin).
OC      Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC      Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC      Strongylocentrotus.
OX      NCBI_TaxID=7668;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Testis;
RA      Galindo B.E., Vacquier V.D.;
RT      "Phylogeny of the TMEM16 Protein Family: Some Are Over Expressed in
RT      Cancer.";
RL      Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; DQ020166; AAY82887.1; -; mRNA.
DR      UniGene; SpU.15325; -.
DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      2: Evidence at transcript level;
SQ      SEQUENCE      921 AA; 106711 MW; C3F912A32528F059 CRC64;

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Query Match 35.8%; Score 1475.5; DB 2; Length 921;

Best Local Similarity 40.4%; Pred. No. 5.2e-114;
Matches 311; Conservative 142; Mismatches 266; Indels 51; Gaps 15;

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Qy      6 DGNTTVHYALLSASWAVLCYYAEDLRKLPLQELPNQASNSAGLLAWLGIPNVLLVEVP 65
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Db     136 DGRT---FFVKVHAPWDLMTTRYAEELKIKMPIEENMEEPVNVFNCIDKLWTFPELSEEEYV 193

Qy     66 DVPPEYYSCRFVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNNLGIHQ 125
      |: :: | :: |: ::|||:| : |: ::::|:| : | || |
Db     194 KPPEPDVFTAPFIRDRASEFI-MESQDTFFPNNI RN RVVYEILERMRYDANDPAKFGIDHL 252

Qy     126 LAEGVLSAAFFLHDGPFFKP-----PEGQAPRLNQRQVL FQHWARWGKWNKYQPLDHVRR 181
      || | |::|:|:|:|:| | | |::|:| | | |::|:| |
Db     253 IANGSYFAAYPLHEGDYKSKHSLTHGPQ----NDRHLLYEEWARPGRWYKKQPLDLIRR 308

Qy     182 YFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC 241
      |||:|:|:| | | | | | | | | | | | | | | | | |
Db     309 YFGEKIGIYFCWLGFYTEMLTWAGFVGLIVFLYGCISLPSSVVQVEICAGTDII-MCPLC 367

Qy     242 -LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLELYWKRSATLAYRWDCSD 300
      ||:| | | : : |||: |||: ||:| | : |:|:|: | : | |
Db     368 DKRCPYWTLSDSCFYSKLTYLFDNEATVFFACFMSLWATMFCFWRKRRQNTIDYDWDLFG 427

Qy     301 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVMCLV 360
      |:| | | | | | :|| | | : | | | : |:|:|: ::
Db     428 FEEQEENIRPEFEAKAPDRRVSPITNLTEPYMKFSRKFPFSASIASIFFMILLVMAAVM 487

Qy     361 SIILYRAIMAVVSRSGNTLLAAWASRIASLTGSSVVNLVFILISKIYVSLAHVLTWRWEM 420
      ::|:| :: : ::::| | | | |::|:| | | | | | | |
Db     488 TVIVYRIVVKTAIFAIDQEFISSYASIITSVTASMISLILIMILQILYERIAVRLTNLEL 547

Qy     421 HRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNHYTLFGV-RNEECAAGG 479
      |||:|:|:|:| |:::| | | | | | | | | | | | | |
Db     548 HRTETEYEDSFTFKMYLFAFVNYSTSFYIAFFKGRLPGTPADYGRVFGWLRQEEDCPAG 607

Qy     480 CLIELAQELLVIMVGKQVINNMQEVLI PKLKGWQKFLRLSKKRKAGASAGASQGPWEDD 539
      |: | : : | | | | | : : | | : : | | : | |
Db     608 CMQELFINIAITMCGKQFNNFMELAMPVLMNFWRS-RTGRKEEKGSGK---GRYEQWEQD 663

Qy     540 YELVPC---EGLFDEYLEMVLQFGFVTIFVAACPLAPL F ALLNNWVEIRLDARKFVCEYRR 597
      : | | | | | | | | | | | | | | | | | | | | |
Db     664 ADLADLGRPLFKEYLEMVVGFGFSTIFVAAPLAPL F ALLNNLVEVRLDAYKFIQLRR 723

Qy     598 PVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPR---AYYRWTRAHDLRGFLNF 654
      |||:| | | | | | : : |:|:|:| | | | | | | |
Db     724 PVAKRAQDIGAWYAILVTGNLSVLTNALVIAFTSEFIPRQVFKYYGGPEATLNGYTNW 783

Qy     655 TLA-----RAPSSFAAAHNRT-----CRYAFRDDDGHSYQT--YW 688
      : | : | | | | | | | | | | | | | | | | |
Db     784 SLSYFNTVDMQNSDKPTDPSYPRVGDEDTDPNYGLNVSVCRYRGNYDE--HYNVTLDYW 841

Qy     689 NLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYLLAKQAL 738
      :::|:| | | | | | : : |:|:| | : : | | | |
Db     842 LVIAIKLAFILLYEHVFLFTKFFVAYIIPDMPEFVKQIKRETYLQQAAL 891

```


Db 262 PMVLDKSAFPELEESDCYTPGFSRARIHHFI--INNKTDTFFSNATRSRIVYHMLERTKYEN 320

Qy 113 GHEKKNLLGIHQLLAEGVLSAAPFLHDGPFTK----PPEGPQAPRLNQRQVLFQHWARWG 168
| | :|| :| | ||| |:|| :|| | | :|| :|||

Db 321 GISK---VGIRKLITNGSYIAAFPPEGAYKSSLPKITHGPQ---NNRHLLYERWARWG 373

Qy 169 KWNKYQPLDHWRRYFGEKVAFYFALWGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQEL 228
| :||| :| |||| :||| :||| :||| | | : :||:

Db 374 MWYKHQPLDLIRMYFGEKIGLYFAWLWYTGMLIPAAVVGCLVCFYFGLVMTNESQVSQEI 433

Qy 229 CGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKR 287
| : : | ||| :| : : | : | ||:|||||:||||| : ||:|

Db 434 CKATEVF-MCPLCDKNCSLQRLNDSICIYAKVTYLFNDGGTVFFAIFMAIWATVLEFVWKR 492

Qy 288 KSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSV 346
: : | ||| :| :| ||| | | : ||| :| :

Db 493 RRSILTYTDLIEWEEEEETLRPQFEAKYYRMEVINPITGKPEHPQSSDKVTRLLVSVS 552

Qy 347 VIVVMVAVVMCLVSIILYR-AIMAIVVSRSNGTLLAAWASRIASLTGVS-VNLVFILIL 404
| :||: : : :|| :| | | : : : :| :| :| :

Db 553 GIFFMISLVITAVFAVVYRLVVMQFASFKNFVKQHW--QFATSGAAVCINFIIIMLL 610

Qy 405 SKIYVSLAHVLRWEMHRTQTKFEDAFTLKVFIQFVNIFYSSPVYIAFFKGRFVGYPGNY 464
: | :||| | ||:|:|:| ||:|:| | | ||| ||||:| |

Db 611 NLAYEKIAYLLTNLEYPRTSEWENSFALKMFLQFVNLNSSIFYIAFFLGRFVGHGPKY 670

Qy 465 HTLF-GVRNEECAAGGCLIELAQELLVIMVGQVINNMQEVLIPLKLGWQKFLRLRSKR 523
: || | || ||||:| :| || ||: | :| :| :| :

Db 671 NKLFERWRLEECHPSGCLIDLCLQMGVIMFLKQIWNFMELGYPLIQNWWSRHKI----- 725

Qy 524 KAGASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAAACPLAPLALLNNW 581
| | | | :| :| | | || ||||| |||| | ||| ||||

Db 726 KRGIQ-DASIPQWENDWNLQPMNIHGLMDEYLEMVLQFGFTTIFVAAFPLAPLALLNNI 784

Qy 582 VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYYR 641
:||||| || :||| :| |||| | | :| ||||:|:| :||:| |

Db 785 IEIRLDAYKFVTQWRRLPARATDIGIWLGLEIGILAVITNAFVIAITSDYIPRFVYE 844

Qy 642 W-----TRAHDLRGFLNFTLARAP-SSFAAAHNRTCryRAFR-----DDDGHSYQ 685
: : :|:| :| :| | : ||| :| : :

Db 845 YKYGPCANHVKNENCLKGYVNNSLFFDLSELGMKSGYCRYRDRGPPWSSSKPYEFTL 904

Qy 686 TYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQALAEVLF 745
||:| ||| :|||:| : : :||| : : :|| | : : | :

Db 905 QYWHILAAARLAFIIVFEHLVFGIKSFIAYLIPDIPKGLRERIRREKYLVQEMMYEAE-- 962

Qy 746 GTNGTKDEQPKGSELSSHW 764
: : : | : |

Db 963 -EHLQQQRRKSGQPIHHEW 980

RESULT 9

TM16C_HUMAN

ID TM16C_HUMAN

AC Q9BYT9;

Reviewed;

981 AA.

DT 16-JAN-2004, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-2001, sequence version 1.
 DT 24-JUL-2007, entry version 31.
 DE Transmembrane protein 16C.
 GN Name=TMEM16C; Synonyms=C11orf25; ORFNames=GENX-3947;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Rosier M.F., Toselli E., Segurens-Soury B., Auffray C., Devignes M.D.;
 RT "Predominant brain expression and full-length characterization of a
 RT novel human 6.6-Kb transcript mapping at 11p14 in the telomeric part
 RT of WAGR locus."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein
 CC (Probable).
 CC -!- SIMILARITY: Belongs to the TMEM16 family.
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 CC -----
 DR EMBL; AJ300461; CAC32454.1; -; mRNA.
 DR UniGene; Hs.91791; -.
 DR Ensembl; ENSG00000134343; Homo sapiens.
 DR KEGG; hsa:63982; -.
 DR HGNC; HGNC:14004; TMEM16C.
 DR MIM; 610110; gene.
 DR PharmGKB; PA25489; -.
 DR ArrayExpress; Q9BYT9; -.
 DR InterPro; IPR007632; DUF590.
 DR PANTHER; PTHR12308; DUF590; 1.
 DR Pfam; PF04547; DUF590; 1.
 PE 2: Evidence at transcript level;
 KW Membrane; Transmembrane.
 FT CHAIN 1 981 Transmembrane protein 16C.
 FT /FTId=PRO_0000072565.
 FT TRANSMEM 398 420 Potential.
 FT TRANSMEM 471 490 Potential.
 FT TRANSMEM 553 575 Potential.
 FT TRANSMEM 590 612 Potential.
 FT TRANSMEM 642 664 Potential.
 FT TRANSMEM 759 781 Potential.
 FT TRANSMEM 809 831 Potential.
 FT TRANSMEM 904 926 Potential.
 SQ SEQUENCE 981 AA; 114655 MW; 15A3276420912393 CRC64;

Query Match 35.6%; Score 1467.5; DB 1; Length 981;
 Best Local Similarity 40.9%; Pred. No. 2.6e-113;
 Matches 313; Conservative 149; Mismatches 245; Indels 59; Gaps 21;

Qy 20 WAVLCYYAEDLRLLKLPLQ-----ELPNQASNWSAGLLAWLGIPNVLL--VVPDV 67
 | || ||| | ::| : : : : | : ::| ||:
 Db 214 WDTLCKYAERLNIRMPFRKKCYITDGRSKSMGRMQTYFRRIKDWMAQNPMVLKSAFPDL 273

Qy 68 -PPEYYSCRFVKNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GHEKKNLLGIHQ 124
 Db 274 EESDCYTGFPSRARIHHFI-INNKDTFFSNATRSRIVYHMLERTKYENGISK---VGIRK 329

Qy 125 LLAEGVLSAAPPFLHDGPFKT----PPEGQAPRLNQRQVLFQHWARWGKWNKYQPLDHR 180
 Db 330 LINNGSYIAAPPHEGAYKSSQPIKTHGPQ---NNRHLLYERWARWGMWYKHQPLDLIR 385

Qy 181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSIDIPTQELCGSKDSFEMCPL 240
 Db 386 LYFGEKIGLYFAWLGWYTGMLIPAAIVGLCVFFYGLFTMNSQVSQEICKATEVF-MCPL 444

Qy 241 C-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKATLAYRWDCS 299
 Db 445 CDKNCSLQRLNDSICIYKVTYLFNNGGTVFFAIFMAIWAIVLEFWKRRRSILTYTWDLI 504

Qy 300 DYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMC 358
 Db 505 EWEETELRPQFEAKYKMEIVNPITGKPEHPQSSDKVTRLVSVSGIFFMISLVITA 564

Qy 359 LVSIIYLR-AIMAVVSRSGNTLLAAWASRIASLTGSV-VNLVFIILSKIYVSLAHVLT 416
 Db 565 VFGVVYRLVVMQFASFKWFIKQYW--QFATSAAVCFINFIIIMLLNLAYEKIAYLLT 622

Qy 417 RWEMHRTQTKFEDAFTLVKVFIFQVNFYSSPVYIAFFKGRFVGYPGNYHTLFG-VRNEEC 475
 Db 623 NLEYPRTESEWENSFALKMFLFQFVNLNSSIFYIAFFLGRFVGHGPKYKNLFDWRWRLEEC 682

Qy 476 AAGGCLIELAQELLVIMVGQVINNMQEVLLIPKLKGWQKFLRLSKRRKAGASAGASQGP 535
 Db 683 HPSGCLIDLCLQMGVIMFLKQIWNFMELGYPLIQNWWSRHKI-----KRGH-DASIPQ 736

Qy 536 WEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPLALLNNWVEIRLDARKFVC 593
 Db 737 WENDWNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAPLAPLALLNNIIEIRLDAYKFVT 796

Qy 594 EYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYYRW-----T 643
 Db 797 QWRRPLPARATDIGIWLIGILEGIGILAVITNAFVIAITSDYIPRFVYKEYGPCANHVEP 856

Qy 644 RAHDLRGLNFTLARAP--SSFAAAHNRTCRYRAFR----DDGHYSQTYWNLLAIRLAF 697
 Db 857 SENCLKGYVNSLSFFDLSELGMGKSGCYRYDRYGPWSSKPYEFTLQYWHILAAARLAF 916

Qy 698 VIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQALANEV 743
 Db 917 IIVFEHLVFGIKSFIAYLIPDVPKGLHDIRREKYLQVEMMYEAE 962

RESULT 10

A1A5Z4_DANRE

ID A1A5Z4_DANRE Unreviewed; 900 AA.

AC A1A5Z4;

DT 23-JAN-2007, integrated into UniProtKB/TrEMBL.

DT 23-JAN-2007, sequence version 1.
 DT 24-JUL-2007, entry version 6.
 DE Zgc:158430.
 GN ORFNames=zgc:158430;
 OS Danio rerio (Zebrafish) (Brachydanio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 TX TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RG NIH MGC Project;
 RL Submitted (DEC-2006) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; BC128870; AAI28871.1; -, mRNA.
 DR UniGene; Dr.108272; -.
 DR ZFIN; ZDB-GENE-061215-108; zgc:158430.
 DR InterPro; IPR007632; DUF590.
 DR PANTHER; PTHR12308; DUF590; 1.
 DR Pfam; PF04547; DUF590; 1.
 PE 2: Evidence at transcript level;
 SQ SEQUENCE 900 AA; 105263 MW; DB86567CCE3D153E CRC64;

Query Match 35.5%; Score 1463; DB 2; Length 900;
 Best Local Similarity 39.0%; Pred. No. 5.6e-113;
 Matches 308; Conservative 159; Mismatches 244; Indels 78; Gaps 18;

Qy 12 HYALLSASWAVLCYYAEDLRKLPL-----QELPNQASNWSAGLLAWLGIPNVLLV 63

Db	98	HYLKIHPWEVLATYADVLRKIKVPFKVSDIPKAREVP-----LEWLSHPFRLPEN	147
Qy	64	VPDVPPEYYSCRFVRNKLPRFLGSDNQDTFTTSTKRHQILFEILAKTPYGHG---KKNLL	120
Db	148	IMRPEPDYFTAPFDKSKVDFFL-IDDKDTFFPPSTRNRIVYYILTRCPYYKEDRKEKDKT	206
Qy	121	GIHQLLAEGVLSAAFPPLHDGPFKTPPEGQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR	180
Db	207	GINRLNNGTYTSAYPLHDCRYWKAQDMQCE--SERYHLRYWARFLCFYKEQPLNLIK	264
Qy	181	RYFGEKVYALFYAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSK--DSFEMC	238
Db	265	KYYGEKIGIYFAWLGFYTEMLFYAAVMGVICFVYGVLSYEDNITSKEICDPKIGGMIVMC	324
Qy	239	PLC-LDCPFWLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLEYWKRKSATLAYRWD	297
Db	325	PLCDKKCSYWKLNSTCLSSWQSHLFDNEGTVFFAMFGIWWTLFLEFWKRRQARLEYEWD	384
Qy	298	CSDYEDTEE--RPRPQFAASAPMTAPNPITGEDEPYFFPERSRARRMLAGSVVIVVMVAVV	355
Db	385	LVDFFFFEQQLQIRPEYEQKCTGRRLNRITQEMEPYLPFPFSKCARFCLSGATVLFWTCLI	444
Qy	356	VMCLVSIIILYR----AIMAIVVSRSGNTLLAAWASRI-----ASLTGSVVNLVFILILSK	406
Db	445	VACIMGVIAYRLAVYAFAFASVMKDSSTSКИQVGLSLITPQLATSVTASCINFEVILILNF	504
Qy	407	IYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHT	466
Db	505	LYEHVAIWITDMEIPKTHLEYENKLTMKMFMFQFVNYSSCFYVAFKKGKFGVGYPGNYSY	564
Qy	467	LFG----VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPLKLGWQKFRLSKK	522
Db	565	MFGKSWTLRNEECAPGGCLIELTTQLLIVMAGKQMVGNVQEALLPLVRNWW-----SS	617
Qy	523	RKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPLALLNN	580
Db	618	RKGRSHPESTYSRWEDQHDHLQNFSSQFGLFYEYLEMVIQFGFITLFVASFPLAPLALLFNN	677
Qy	581	WVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPR---	637
Db	678	ILEVRVDWKFTTQFRPFMAAKARNIGAWEEILNVVAIMSVVTNAFIMAFITSDMIPRLVY	737
Qy	638	--AYYRWTRAHDLRGLNFTLA-----RAPSSFAAAHNRTCRYRAFRDD	679
Db	738	LYAYHPGIEA-NMTGYITNSLSIYNISQIPEDNLPEAGENPSWFSNSTIITCRYRDIYRP	796
Qy	680	DGH---YSQT--YWNLLAIRLAFVIVFEHVVSVGRLLDLLVPDIPESVEIKVKREYYLA	734
Db	797	PGHLRQYTHTMQFWHILAAKLAFIIMEHVVVVVKFFVAVWLIPDVPSEVKARIKRERFLV	856
Qy	735	KQALAENEV	743
Db	857	QEYLHNYEV	865

RESULT 11

Q1AP37_STRPU

ID Q1AP37_STRPU Unreviewed; 921 AA.
 AC Q1AP37;
 DT 11-JUL-2006, integrated into UniProtKB/TrEMBL.
 DT 11-JUL-2006, sequence version 1.
 DT 24-JUL-2007, entry version 6.
 DE 122 kDa protein TMEM16.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Galindo B.E., Moy G.W., Vacquier V.D.;
 RT "A 122 kDa protein from Strongylocentrotus purpuratus embryo belongs
 RT to TMEM16 protein family."
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; DQ020164; AAY82885.1; -, mRNA.
 DR UniGene; Spu.15325; -.
 DR InterPro; IPR007632; DUF590.
 DR PANTHER; PTHR12308; DUF590; 1.
 DR Pfam; PF04547; DUF590; 1.
 PE 2: Evidence at transcript level;
 SQ SEQUENCE 921 AA; 106699 MW; 9A516A5DCA1ADCCC CRC64;

Query Match 35.4%; Score 1460.5; DB 2; Length 921;
 Best Local Similarity 40.1%; Pred. No. 9.4e-113;
 Matches 309; Conservative 140; Mismatches 270; Indels 51; Gaps 15;

Qy 6 DGNTTVHYALLSASWAVLCYYAEDLRKLPLQELPNQASNSAGLLLAWGIPNVLLLEVVP 65
 || | : : | | : : |||:|:|:|:| : : | | |
 Db 136 DGRT--FFVKVHAPWDLMTYAEELKIKMPIEENNMEEPVNVCIDKLWTPFELSEEYV 193

Qy 66 DVPPEYYSCRFVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQ 125
 | : : : | : : | : : |||| : | : : : || : | || |
 Db 194 KPEPDVFTAPFIRDRASEFI-MESQDTFFPNNIRNRVVEILERMRYDANDPTKFGIDHL 252

Qy 126 LAEGVLSAAFLPHDGFPKTP----PEGPQAPRLNQRQVLQFQHWARWGKNKYQLDHHVR 181
 : | | ||:|:|:| : : || | | : : || | : | | || : |
 Db 253 IANGSYFAAYPLHEGDYKSKHSLLTHTGPQ----NDRHLLYEAWRSGRWYKKQPLDLIRC 308

Qy 182 YFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSIDIPTQELCGSKDSFEMCPLC 241
 |||| : | | |||| | | | : || | : | : | : | | || |
 Db 309 YFGEKIGIYFCWLGIFYTEMLTWAGFVGLIVFLYGCISLPSVVVEICAGTDII-MCPLC 367

Qy 242 -LDCPFWLLSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCCSD 300
 || : | | : : ||| : ||| : | : ||| : | : | |
 Db 368 DKRCPYWTLSDSCFYSKLTYLFDNEATVFFACFMSLWATMFCFVKRRQNTIDYDWDLFG 427

Qy 301 YEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSARRMLAGSVVIVVMVAVVMCLV 360
 Db 428 FEEQEENIRPEFEAKAPDRRVSPTNLPEQYMKFSKRFPFRFSTSVPTIAFMILLVMAVM 487

Qy 361 SIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSSVNNLVFILILSKIYVSLAHVLTREW 420
 Db 488 TVIVYRIVVKTAIFAIDQEFITSSYAIITSVTASMIILIMILQILYERIAVWLTNLEL 547

Qy 421 HRTQTKFEDAFTLKVFIQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGV-RNEECAAGG 479
 Db 548 HRTETEYEDSFTFKMYLFAFVNYYSSTSFYIAFFKGRLPGPADYGRVFGIWRQEEDPAG 607

Qy 480 CLIELAQELLVIMVGKQVINNMQEVLPKLGWQKFLRLSKRRKAGASAGASQGPWEDD 539
 Db 608 CTQELFINIAITMCGKQFFNNFMELAMPVLMNFWRS-RTGRKEEKS GK---GRYEQWEQD 663

Qy 540 YELVPC---EGLFDEYLEMVLQFGFVTIFVAACLAPLAFALLNNWVEIRLDARKFVCEYRR 597
 Db 664 ADLADLGRPLFKYLEMVMVQFGFSTIFVAAFPLAPLAFALLNNLVEVRLDAYKFIQLRR 723

Qy 598 PVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPR---AYYRWTRAHDRLGRFLNF 654
 Db 724 PVAKRAQDIGAWYAILVTGNLSVLTNALVIAFTSEFIPRQVFKYGGPEATLNGYTNW 783

Qy 655 TLA-----RAPSSFAAAHNRT-----CRYRAFRDDDGHSYQT--YW 688
 Db 784 SLSYFNTVDMQNDKSKPTDPSYPRVGDEDTTDPNYGLNVSVCRYRGNYDE--HYNVTLDYW 841

Qy 689 NLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQAL 738
 Db 842 LVIAIKLAFILLYEHFVLTKFFVAYIIPDMPEFVKVQIKRETYLGQQAL 891

RESULT 12

TM16A_MOUSE

ID TM16A_MOUSE Reviewed; 960 AA.
 AC Q8BHY3; Q6P5C6; Q8BI26; Q99JK1;
 DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.
 DT 29-MAY-2007, sequence version 2.
 DT 24-JUL-2007, entry version 32.
 DE Transmembrane protein 16A.
 GN Name=Tmem16a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Head, and Kidney;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,

RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC STRAIN=C57BL/6, and Czech II; TISSUE=Eye, and Mammary tumor;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA
RT project: the Mammalian Gene Collection (MGC).";
RL Genome Res. 14:2121-2127(2004).
CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein
CC (By similarity). Cytoplasm (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8BHY3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8BHY3-2; Sequence=VSP_025672;
CC -!- SIMILARITY: Belongs to the TMEM16 family.
CC -!- SEQUENCE CAUTION:
CC Sequence=BAC35051.1; Type=Miscellaneous discrepancy; Note=Wrong choice of frame;
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

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CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AK028991; BAC26230.1; ALT_INIT; mRNA.
DR      EMBL; AK029329; BAC26398.1; ALT_INIT; mRNA.
DR      EMBL; AK052589; BAC35051.1; ALT_SEQ; mRNA.
DR      EMBL; BC006062; AAH06062.1; ALT_INIT; mRNA.
DR      EMBL; BC062959; AAH62959.1; -; mRNA.
DR      UniGene; Mm.26700; -.
DR      Ensembl; ENSMUSG00000031075; Mus musculus.
DR      MGI; MGI:2142149; Tmem16a.
DR      ArrayExpress; Q8BHY3; -.
DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      2: Evidence at transcript level;
KW      Alternative splicing; Cytoplasm; Glycoprotein; Membrane;
KW      Transmembrane.
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FT                                     /FTId=PRO_0000288436.
FT      TOPO_DOM        1          333          Cytoplasmic (Potential).
FT      TRANSMEM        334          354          Potential.
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FT      TRANSMEM        403          423          Potential.
FT      TOPO_DOM        424          493          Cytoplasmic (Potential).
FT      TRANSMEM        494          514          Potential.
FT      TOPO_DOM        515          539          Extracellular (Potential).
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FT      TOPO_DOM        561          581          Cytoplasmic (Potential).
FT      TRANSMEM        582          602          Potential.
FT      TOPO_DOM        603          705          Extracellular (Potential).
FT      TRANSMEM        706          726          Potential.
FT      TOPO_DOM        727          765          Cytoplasmic (Potential).
FT      TRANSMEM        766          786          Potential.
FT      TOPO_DOM        787          856          Extracellular (Potential).
FT      TRANSMEM        857          877          Potential.
FT      TOPO_DOM        878          960          Cytoplasmic (Potential).
FT      CARBOHYD        806          806          N-linked (GlcNAc..) (Potential).
FT      VAR_SEQ         448          451          Missing (in isoform 2).
FT                                     /FTId=VSP_025672.
SQ      SEQUENCE      960 AA;  110916 MW;  BFD0112FD310CE88 CRC64;

Query Match          35.2%; Score 1452.5; DB 1; Length 960;
Best Local Similarity 40.0%; Pred. No. 4.6e-112;
Matches 330; Conservative 156; Mismatches 257; Indels 81; Gaps 22;

Qy      6  DGNTTVH---YALLSASWAVLCYYAEDLRLLKPLQELPNQASNWSAGLLAWLGIPNVLL 62
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Db      145 DEDTKIHGVGVFKIHAPWHVLCREAEFLKLMPTKKVYHISE--TRGLLK--TINSVLQK 200

Qy      63  VVPDPVPEYYSCFRFRVKNLPRFLGS-----DNQDTFFTSTKRHQILFEILAKTPYG 113
      : : | : : | : | : | : | : | : | : | : | : | : | : |
Db      201 ITDPIQPKVAEHRPQTTRKLSYPFSREKQHLFDLTDSDFFDSKTRSTIVYEILKRTTCT 260

Qy      114 HEKKNLLGIHQLLAEGVLSAAPFLHDGPFKTPPEGPQAPRLNQRQVLQFQHWARWGKWNKY 173
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DE amplified and overexpressed sequence 2).

GN Name=TMEM16A; Synonyms=DOG1, ORAOV2, TAOS2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

OC Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.

RX PubMed=16906560; DOI=10.1002/gcc.20371;

RA Huang X., Godfrey T.E., Gooding W.E., McCarty K.S. Jr., Gollin S.M.;

RT "Comprehensive genome and transcriptome analysis of the 11q13 amplicon

RT in human oral cancer and syntenic to the 7F5 amplicon in murine oral

RT carcinoma.";

RL Genes Chromosomes Cancer 45:1058-1069(2006).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).

RC TISSUE=Testis;

RX PubMed=14702039; DOI=10.1038/ng1285;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto Y., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,

RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,

RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,

RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,

RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,

RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,

RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,

RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Togashi T., Oyama H., Hata H., Watanabe M., Komatsu T.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

RT "Complete sequencing and characterization of 21,243 full-length human

RT cDNAs.";

RL Nat. Genet. 36:40-45(2004).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).

RC TISSUE=Testis;

RX PubMed=15489334; DOI=10.1101/gr.2596504;

RG The MGC Project Team;

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RT  "The status, quality, and expansion of the NIH full-length cDNA
RT  project: the Mammalian Gene Collection (MGC).";
RL  Genome Res. 14:2121-2127(2004).
RN  [4]
RP  IDENTIFICATION, AND TOPOLOGY.
RX  PubMed=12739008;
RA  Katoh M., Katoh M.;
RT  "FLJ10261 gene, located within the CCND1-EMS1 locus on human
RT  chromosome 11q13, encodes the eight-transmembrane protein homologous
RT  to C12orf3, C11orf25 and FLJ34272 gene products.";
RL  Int. J. Oncol. 22:1375-1381(2003).
RN  [5]
RP  SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX  PubMed=15215166;
RA  West R.B., Corless C.L., Chen X., Rubin B.P., Subramanian S.,
RA  Montgomery K., Zhu S., Ball C.A., Nielsen T.O., Patel R.,
RA  Goldblum J.R., Brown P.O., Heinrich M.C., van de Rijn M.;
RT  "The novel marker, DOG1, is expressed ubiquitously in gastrointestinal
RT  stromal tumors irrespective of KIT or PDGFRA mutation status.";
RL  Am. J. Pathol. 165:107-113(2004).
RN  [6]
RP  SUBCELLULAR LOCATION.
RX  PubMed=16261155; DOI=10.1038/sj.onc.1209203;
RA  Carles A., Millon R., Cromer A., Ganguli G., Lemaire F., Young J.,
RA  Wasylyk C., Muller D., Schultz I., Rabouel Y., Dembele D., Zhao C.,
RA  Marchal P., Ducray C., Bracco L., Abecassis J., Poch O., Wasylyk B.;
RT  "Head and neck squamous cell carcinoma transcriptome analysis by
RT  comprehensive validated differential display.";
RL  Oncogene 25:1821-1831(2006).
CC  -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein.
CC  Cytoplasm.
CC  -!- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=3;
CC  Name=1;
CC  IsoId=Q5XXA6-1; Sequence=Displayed;
CC  Name=2;
CC  IsoId=Q5XXA6-2; Sequence=VSP_025665, VSP_025668, VSP_025669;
CC  Note=No experimental confirmation available;
CC  Name=3;
CC  IsoId=Q5XXA6-3; Sequence=VSP_025666, VSP_025667, VSP_025668,
CC  VSP_025669, VSP_025670, VSP_025671;
CC  Note=No experimental confirmation available;
CC  -!- TISSUE SPECIFICITY: Broadly expressed with higher levels in liver
CC  and skeletal muscle.
CC  -!- SIMILARITY: Belongs to the TMEM16 family.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; AY728143; AAU82085.1; -; mRNA.
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DR  EMBL; BC033036; AAH33036.2; -; mRNA.
DR  UniGene; Hs.503074; -.
DR  Ensembl; ENSG00000131620; Homo sapiens.
DR  HGNC; HGNC:21625; TMEM16A.
DR  MIM; 610108; gene.

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DR PharmGKB; PA128394678; -.
 DR ArrayExpress; Q5XXA6; -.
 DR InterPro; IPR007632; DUF590.
 DR PANTHER; PTHR12308; DUF590; 2.
 DR Pfam; PF04547; DUF590; 1.
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 KW Alternative splicing; Cytoplasm; Glycoprotein; Membrane; Polymorphism;
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 FT TOPO_DOM 904 986 Cytoplasmic (Potential).
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 FT /FTId=VSP_025668.
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 FT /FTId=VSP_025669.
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 FT YLKLKQQSP -> VTEILFISGSFPFCAYDLSTPCTWEKQL
 FT QHICSAKSSRFLSFLLETFLFP (in isoform 3).
 FT /FTId=VSP_025670.
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 FT /FTId=VAR_032417.
 FT VARIANT 983 983 G -> R (in dbSNP:rs3740722).
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 FT CONFLICT 948 948 W -> C (in Ref. 3; AAH33036).
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Query Match 35.2%; Score 1450.5; DB 1; Length 986;
 Best Local Similarity 39.1%; Pred. No. 7.1e-112;
 Matches 335; Conservative 149; Mismatches 255; Indels 117; Gaps 24;

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Qy	62 EVVPDPVPEYYSCR-----FRVNKLPRFLGSDNQDTFTTSTKRHQILFEILAKTP	111
	: : : : : : : : : : : : : : : :	
Dd	200 KITDPIQPKEVAEHRPQTMKRLSYPPFSREKQHFLDLSD-KDSFFDSKTRSTIVYEILKRTT	258
Qy	112 YGHEKKNLLGIHQLLAEGLVSAAFFLHDGPFKTPPEGPOAPRLNQOQVLFQHWARWGKW	171
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Dd	259 CTKAKYS-MGITSLLANGVYAAAYPLHDGDY----NGENVEFNDRKLLYEAWARYGVFY	312
Qy	172 KYQPLDHVRRYFGEKVLYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS	231
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Qy	291 TLAYRWDCSDYEDTEE----RPRPQFAA----SAPMTAPNPITGEDEPYPFPERS----	336
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Qy	337 -RARRMLAG-----SVVIVVMVAVVVMCLVSIILIRAIMAIVVS	374
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Qy	375 RSGNTLLAAWASRIASLTGSVVNLVFIILISKIYVSLAHVLTRWEMHRTQTKFEDAFTLK	434
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Dd	610 AFLCLKFVNSYTFIFYVAFFKGRFVGPRGDYVYIFRSFRMEECAPGGCLMELCIQLSII ML	669
Qy	494 GKQVI-NNMQEVLPKLGKWWQKFLRLSKRRKAGASAGSQGPWEDDYELVPCGLFDEY	552
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Dd	670 GKQLIQNNLFEIGIPKMKKLIRYLKLKQQSPPDHEECVKKRQRYVEDYNLEPPAGLTPEY	729
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Qy	613 LAGLTHLAVISNAFLAFSSDFLPRA--YYRWTRAHLRGFLNFTLARAPSSF-----	663
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RESULT 14

TM16B_HUMAN

ID TM16B_HUMAN Reviewed; 999 AA.
 AC Q9NQ90;
 DT 16-JAN-2004, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-2000, sequence version 1.
 DT 24-JUL-2007, entry version 35.
 DE Transmembrane protein 16B.
 GN Name=TMEM16B; Synonyms=C12orf3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
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 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Retina;
 RA Lorenz B., White K.E., Econs M.J., Strom T.M.;
 RT "Transcripts in l2p13.3";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
 CC !- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein
 CC (Probable).
 CC !- SIMILARITY: Belongs to the TMEM16 family.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AJ272204; CAC01125.1; -; mRNA.
 DR UniGene; Hs.148970; -.
 DR Ensembl; ENSG00000047617; Homo sapiens.
 DR KEGG; hsa:57101; -.
 DR HGNC; HGNC:1183; TMEM16B.
 DR MIM; 610109; gene.
 DR PharmGKB; PA25504; -.
 DR LinkHub; Q9NQ90; -.
 DR ArrayExpress; Q9NQ90; -.
 DR GermOnline; ENSG00000047617; Homo sapiens.
 DR InterPro; IPR007632; DUF590.
 DR PANTHER; PTHR12308; DUF590; 1.
 DR Pfam; PF04547; DUF590; 1.
 PE 2: Evidence at transcript level;
 KW Membrane; Polymorphism; Transmembrane.
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 FT TRANSMEM 535 557 Potential.
 FT TRANSMEM 577 599 Potential.
 FT TRANSMEM 619 641 Potential.
 FT TRANSMEM 746 768 Potential.

FT	TRANSMEM	796	818	Potential.
FT	TRANSMEM	898	920	Potential.
FT	VARIANT	108	108	V -> A (in dbSNP:rs3741903).
FT				/FTId=VAR_021932.
FT	VARIANT	501	501	S -> A (in dbSNP:rs1860961).
FT				/FTId=VAR_020331.
SQ	SEQUENCE	999 AA;	113616 MW;	B9B4F56161AE1B00 CRC64;

Query Match 34.9%; Score 1437; DB 1; Length 999;
 Best Local Similarity 38.7%; Pred. No. 9.8e-111;
 Matches 326; Conservative 161; Mismatches 263; Indels 92; Gaps 23;

Qy	1	QQDVQDGNITT	VHYALLSASWAVLCYYAEDLRLKLPQLQELPNQ-----ASNWSAGLLAW	53
Db	170	EKDLENKSGQSIFVRIHAPWQVLAREAEFLKIKVPTKKEMEYIKAGGSI	AKKFSAL---	226
Qy	54	LGIPNVLLLEVVPDPPEYYSCRFRVKNLP-----RFLGSDNQDFTFT	STRKHQILFEIL	107
Db	227	---QKLSSHLQPRV-PEHSNNMKNNLSYPFSREKMYLYNIQEKDFTFD	NATRSRIVHEIL	282
Qy	108	AKTPYGHEKKNLLGIHQLLAEGVLSAAFPPLHDGPFKTPPEGQAPRLN	QRQVLFQHWAR	167
Db	283	KRTACS-RANNTMGINSLIANNIYEAAYPLHDGEYDSPEDD-----M	NDRLKLYQEWARY	336
Qy	168	GKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLPPAAVVGTLVFLVG	CLVFSDIPTQE	227
Db	337	GVFYKQFQPIDLRKYFGEKIGLYFAWLGLYTSFLIPSSSVIGVIVFLY	GCATIEEDIPSRE	396
Qy	228	LCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFM	ALWAVLLLEYWK	286
Db	397	MCDQQNAFTMCPCLCDKSCDYNNLSSACGTAQASHLFDNPAIVFFSIF	MAWATMFLENWK	456
Qy	287	RKSATLAYRWDCSDYEDTEER----PRQFAA-----SAPMTAPNPIT	----G	326
Db	457	RLQMRGLGYFDLTGIEEEEEERAQHSRPEYETKVREKMLKESNQSAVQ	KLETNTECGDE	516
Qy	327	EDEPYFPERSARRMLAGSVVIVVMVAVVMCLVSIILYRAIMAIVVSRS	SGNTLLAAWAS	386
Db	517	DDDEKLTWKDRFPGYLMNFASILFMIALTFSIVFGVIVYRITTAALS	----L	571
Qy	387	RI---ASLTGSVVNLVFILILSKIYVSLAHVLTWRWEMHRTQTQKFED	AFTLKVVFQFVNF	443
Db	572	NVRVTVTATAVIINLVILDEIYGAIVAKWLTHIEVPKTEQTFEERLIL	KAFLLKFVNA	631
Qy	444	YSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLV	IMVGKQVI-N	501
Db	632	YSPIFYVAFFKGRFVGRPGSYVYVFDGYRMEECAPGGCLMELCQLS	IIMLGKQLIQNNI	691
Qy	502	QEVLPKPLKGWQKFRRLSRKRRKAGASAGA-SQGP--WEDDYELVPCE	GLFDEYLEMVLQ	558
Db	692	FEIGVPKPKK---KLFPRKLKDETEAGETDSAHSKHPEQWDLYSLEPY	TGLTPEYMEMIQ	748
Qy	559	FGFVTITFVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQ	DIGIWFHILAGLTH	618
Db	749	FGFVTLFVASFPPLAPVFAALLNNVIEVRLDAKKFVTELRDPDVRTKD	IGIWFIDILSGIGK	808

Qy 619 LAVISNAFLFASSDFLPYRWTRAHD--LRGFLNFTLA-----RAPSSFAA 665
 :|||::| :|||:| |:: |: | |::| |:: : |
 Db 809 FSVISNAFVIAITSDIFPRLVYQYSYSHNGTLHGfVNHLSFFNVSQLKEGTQPENSQFD 868

Qy 666 AHNRTCRYRAFRD-----DDGHYSQTYWNLLAIRLAFVIVFEHVVFSGRLLDLLVPDIP 720
 : ||:: |: : |: || |: | ||||::|::| : |:| ::|||
 Db 869 QEVQFCRFKDYREPPWAPNPYEFKQYWFILSARLAFVIFQNLVLMFSLVLVDWMIPDIP 928

Qy 721 ESVEIKVKRE-----YYLAKQALAEENEVLFGTNGTKDEQPKGSELSSHWPFTVPKA-S 773
 : ::|| :|| : |::| : |::| : |::| : |::| : |::|
 Db 929 TDISDIKKEKSLLVDFFLKE----EHEKLKLMDEPALRSPGGDRSRRAASSAPSGQS 984

Qy 774 QL 775
 ||
 Db 985 QL 986

RESULT 15

Q8CFW1_MOUSE

ID Q8CFW1_MOUSE Unreviewed; 913 AA.
 AC Q8CFW1;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 24-JUL-2007, entry version 21.
 DE Transmembrane protein 16B.
 GN Name=Tmem16b;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RG NIH MGC Project;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; BC033409; AAH33409.1; -; mRNA.
 DR UniGene; Mm.333398; -.
 DR Ensembl; ENSMUSG00000038115; Mus musculus.
 DR MGI; MGI:2387214; Tmem16b.
 DR GO; GO:0016021; C:integral to membrane; IEA:UniProtKB-KW.
 DR InterPro; IPR007632; DUF590.
 DR PANTHER; PTHR12308; DUF590; 1.
 DR Pfam; PF04547; DUF590; 1.
 PE 2: Evidence at transcript level;
 KW Transmembrane.
 SQ SEQUENCE 913 AA; 104388 MW; CA17DB27D8167F64 CRC64;

Query Match 34.8%; Score 1434.5; DB 2; Length 913;
 Best Local Similarity 39.5%; Pred. No. 1.4e-110;
 Matches 310; Conservative 160; Mismatches 242; Indels 73; Gaps 18;

Qy 1 QQDVQDGNNTVHYALLSASWAVLCYYAEDLRLKLPLOEL-----PNQASNWSAGLLAWL 54
 Db 85 EKDLESKSQGSVFVRIHAPWQVLAREAEFLKIKVPTKKMYEIKAGGSIAKKFSFA-ILQTL 143
 Qy 55 GIPNVLLLEVVPDPPEYYSCRFVKNKL-----RFLGSDNQDTFFFTSTKRHQILFEILA 108
 Db 144 SSP-----LQPRV-PEHSNNRMKNLSYFPSREKMYLNIQEKDTFFDNATRSRIVHEILK 197
 Qy 109 KTPYGHEKKNLLGIHQLLAEGVLSAAFPPLHDGPFKTPPEGQPAPRLNQRQVLQFHWARWG 168
 Db 198 RTACS-RANNTMGINSLIANNIYEAAYPLHDGEYDSPGDD-----MNDRKLLYQEWARYG 251
 Qy 169 KWNKYQPLDHWRRYFGEKVALYFAWLGFYTGWLLPAAVVVGLTVFLVGCFLVFSDIPTQEL 228
 Db 252 VFYKFPQIDILIRKYFGEKIGLYFAWLGLYTSFLIPSSVIGVIVFLYGCATIEEDIPSKEK 311
 Qy 229 CGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFHDGGTVFFSLFMALWAVLLLEYWKR 287
 Db 312 CDHQNAFTMCPLCDKSCDYWNLSACGTARASHLFDNPATVFFSIFMALWATMFLENWKR 371
 Qy 288 KSATLAYRWDCSDYEDTEER-----PRPQF-----AASAPMTAPNPITGE-D 328
 Db 372 LQMRLEGYFWDLTGIEEEERSQEHSRPEYETKVREKLLKESGKSAVQKLEANSPEDEDD 431
 Qy 329 EPYFPERSRRARMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAWASRI 388
 Db 432 EDKLTWKDRFPGYLMNFASILFMIALTFISIVFGVIVYRITAAALS-----LNKATRSNV 486
 Qy 389 ---ASLTGSVVNLVFIILSKIYVSLAHVLRWEMHRTQTKFEDATLKVFIQFVNFYS 445
 Db 487 RVTVTATAVINLVILDEIYGAVAKWLTKIEVPKTEQTFEERLILKAFLLKFVNAYS 546

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